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FIGURE 1

Domain	Start	End	Bits	Evalue	Alignment
7tm_1	59	314	140.30	1e-43	Align

[358 residues]
7tm_1 59-314

Alignments of Pfam-A domains to HMMs

Format for fetching alignments to seed [\[Hyperlinked to swisspfam\]](#)

Alignment of 7tm_1 vs UserSeq/59-314

```
*->GNLLVilvilrtkkrlrtptnifilMLAvADLLflltppwalyylvg
N+L+++++ + +t++ ++ N vADL ++lt p+ ++ + +
UserSeq 59  LNGLAVWIFFH-IRNKTSFIFYLKNIIVADLIMTLTFPFRIVHDAGF 104

gsedWpfGsalCklvtaldvvnmyaSi111taISiDRYIAIvhPlryrrr
g W f +lC+ ++ l+++nny+Si +L +ISiDRYl ++P+ ++r+
UserSeq 105 G--PWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYLKVVKPFQDSRM 152

rtsprrrAkvvillvWvlal11slPpllfswvktveegngtlnvntvCli
++ +kv++++vWv+ ++lslP +++ + ++ e++ ++ C+
UserSeq 153 YS-ITFTKVL SVCYVWVIMAVLSLPNIILTNGQPTEDN-----IHDCSK 194

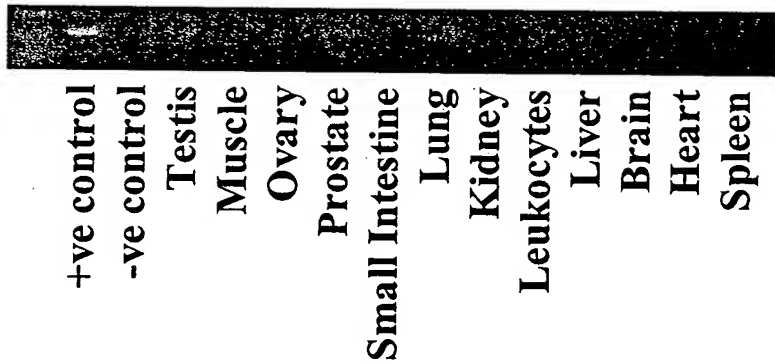
dfpeestasvstwlrsvyllstlvglFllPl1lvilvcYtrIlrtlr.....
+ + + v++ + + F+ l++++ cY I r ++++++
UserSeq 195 LKSP1GV-----KWHYAVTVVNSCLFVAVLVILIGCYIAISRYIHkssrq 239

.....kaaktllvvvvvFv1CWlPyfivllldtlo.lsiimsstCe
++++++k + vvv vF+ C+lPy++ + +t+ +l+ ++ +
UserSeq 240 f1sqssrkrKHNSIRVVVAFFTCFLPYHLCRIPFTFSbLDR--LLDES 287

lervlptallvtlwLayvNsc1NPi1Y<-+
++l + + +tl+L+ +N cl+Pi1Y
UserSeq 288 AQKILYYCKEITLFLSACNVCLDPI1Y 314
```

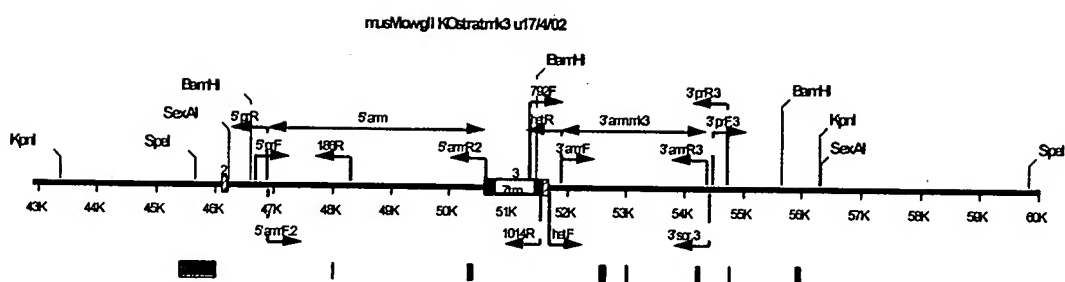
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FIGURE 2



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FIGURE 3



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FIGURE 4

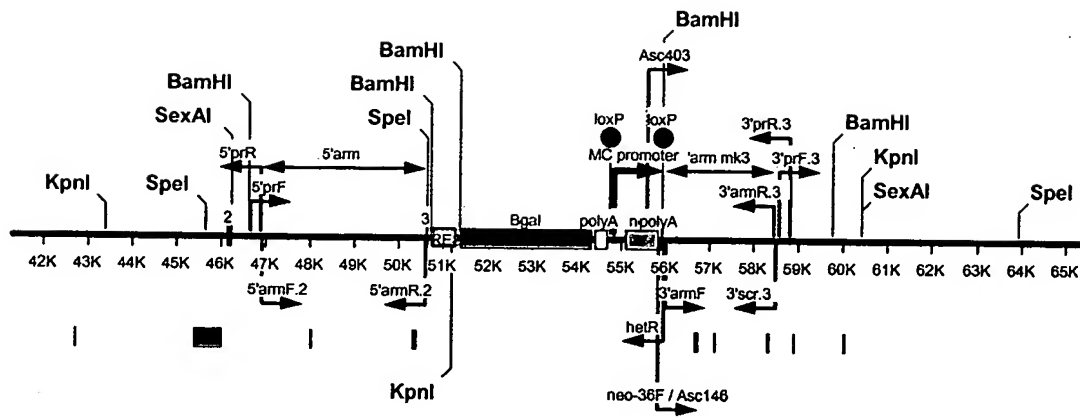


FIGURE 5

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